Program and Abstracts

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Plant resistance-driven emergence of recombinant begomoviruses

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Abstract

The analysis of plant virus genomes reveals that many were shaped by recombination. However, the history of the emergence dynamics of these recombinants is mostly unknown as well as the underlying evolutionary forces that drove their frequency increase. The pivotal role of recombination in geminivirus evolution is supported by the detection of numerous recombination events in sequence data, and by their high propensity to recombine. These typical features were observed with Tomato yellow leaf curl virus (TYLCV), a tomato begomovirus that was extensively studied because of its global economic importance. TYLCV-IS76 is a recombinant TYLCV detected initially in Morocco. It inherited a 76-nt region of tomato yellow leaf curl Sardinia virus (TYLCSV) starting from the origin of replication (OR) towards the V2 gene. Based on field surveys carried out in Morocco and laboratory analysis, a real time emergence of TYLCV-IS76 has been reconstructed from its generation to the displacement of its parental viruses (1). Its emergence coincided with the deployment of Ty-1 resistant tomato cultivars, and a causal link was demonstrated with various competition tests in which positive selection of TYLCV-IS76 was observed in Ty-1 resistant plants (2). TYLCV-IS141 is a TYLCV recombinant detected in Italy (1, 3, 4, 5). It inherited a 141-nt region of TYLCSV between OR and the initiation codon of the V2 gene. TYLCV-IS141 and TYLCV-IS76 exhibit similar recombination profiles and fitness phenotypes in Ty-1 resistant plants. It was inferred from competition tests carried out with various natural and artificially generated TYLCV-IS76 and TYLCV-IS141 clones, that the fitness phenotype of these recombinants was determined by new beneficial intra genomic interaction rather than by a direct effect of specific mutations. Gene silencing is suspected to be involved in the positive selection of these recombinants because Ty-1 is a RNA dependent RNA polymerase gene.

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(4) Granier et al., 2019. Plant Disease.
(5) Panno, et al., 2018. Archives of Virology 163, 795-797.